

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:23:54 ; Search time 11.5226 Seconds

(without alignments)
3287.177 Million cell updates/sec

Title: US-09-836-077-4

Perfect score: 2120

Sequence: 1 MTPPPGGAAPSAPRARVLS.....TFQVADSHPEVAQRVEPMGP 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	907.5	42.8	653	2 T03102	semaphorin homolog
2	368	17.4	749	2 G01856	semaphorin V - hum
3	363	17.1	771	2 D49423	semaphorin III pre
4	361.5	17.1	748	2 I48744	semaphorin A - mou
5	355.5	16.8	782	2 I48746	semaphorin C - mou
6	350	16.5	772	2 A49069	collapsin - chicke
7	349	16.5	772	2 I48747	semaphorin D - mou
8	341.5	16.1	441	2 S29921	hypothetical prote
9	340.5	16.1	403	2 E42521	A39r protein - vac
10	331.5	15.6	751	2 I48748	semaphorin E - mou
11	329.5	15.5	666	2 I58169	semaphorin III - m
12	327.5	15.4	753	2 G02173	semaphorin III fam
13	314	14.8	834	2 S66498	M-sema F protein p
14	312	14.7	730	2 JH0798	fasciclin IV precu
15	298	14.1	711	2 A49423	semaphorin I precu
16	296.5	14.0	712	2 T27165	hypothetical prote
17	287.5	13.6	760	2 I48745	semaphorin B - mou
18	274.5	12.9	1074	2 JC5928	semaphorin F precu
19	264	12.5	724	2 C49423	semaphorin II prec
20	260	12.3	656	2 B49423	semaphorin I - fru
21	217.5	10.3	295	2 JQ1775	Sa19r protein - v
22	186	8.8	676	2 T33853	hypothetical prote
23	131	6.2	620	2 T30765	hypothetical prote
24	121	5.7	2051	2 T13164	plexin B - fruit f
25	113	5.3	1894	2 JC4980	plexin 1 precursor
26	110.5	5.2	122	2 C72169	A46r protein - var
27	110.5	5.2	122	2 H36852	A43r protein - var
28	110.5	5.2	122	2 T28584	14R protein - vari
29	110.5	5.2	1375	1 JC5148	hepatocyte growth

30	109.5	5.2	1945	2 T13937	plexin A - fruit f
31	102	4.8	142	2 JQ1776	Sa19r protein - v
32	102	4.8	399	2 T40831	probable guanine n
33	99	4.7	1948	2 B69511	N conserved hypoth
34	98.5	4.6	929	2 T35683	ftsk homolog - Str
35	98.5	4.6	1905	2 I51553	plexin - African c
36	98	4.6	407	2 H69064	serine/threonine p
37	97	4.6	987	2 D97029	ribonucleotide red
38	97	4.6	1884	2 JC4975	plexin 2 precursor
39	97	4.6	4351	2 T00252	MEGF1 protein - ra
40	96.5	4.6	1272	2 F97568	hypothetical prote
41	96.5	4.6	1272	2 AF2789	hypothetical prote
42	95	4.5	528	2 S2431	abrin-d precursor
43	94.5	4.5	528	1 TZLSA	abrin-a precursor
44	94.5	4.5	903	2 E88221	protein T01H3.2 [1
45	93	4.4	518	2 T23120	hypothetical prote

ALIGNMENTS

RESULT 1

T03102

semaphorin homolog A3 - alcelaphine herpesvirus 1

C:Species: alcelaphine herpesvirus 1

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999

C:Accession: T03102

R:Ensser, A.; Pflanz, R.; Fleckenstein, B.

J. Virol. 71, 6517-6525, 1997

A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.

A:Reference number: Z14840; MUID:97404659; PMID:9261371

A:Accession: T03102

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-653 <ENS>

A:Cross-references: EMBL:AF005370; NID:g2337967; PIDN:AAC58054.1; PID:g2337970

Query Match 42.8%; Score 907.5; DB 2; Length 653;
Best Local Similarity 48.9%; Pred. No. 1.7e-68;
Matches 182; Conservative 54; Mismatches 129; Indels 7; Gaps 5;

QY	22	PARFG-LPLRLLLVFWAAASAGHSRSGPRISAVWK---QGDHVDVFSQPEPHVLFH	77
DB	45	PRAMGTLCSVIRLLML-SAITAKSRFDKPLIYNLTDGFGQ-HRFEGQPEPHVLFH	102
QY	78	EPGSFVWVGGRGVYHFNPECKNASVTVTNGTSGQDKQDCGNYITLLRRNGL	137
DB	103	SLNSSDVYVGGNTIYLFDFAHSSNASTALINITSTHNRSLSTCENFTLLHNQTDGL	162
QY	138	LYCGTNARKPSCHNLVNDVMSLGEMKGVAPSPDENSLVLFEGDEVYSTIRKQEVNGK	197
DB	163	LACGTSNQKPSCH-LINNTTQFLGPKLGLAPSPSGNLVLFQDNTYSTINLYKSLG	221
QY	198	IPRFRIRGESELYTSDTVNQNPQFIKATIVHQDQYDDKIYFFREDNPKRPEALNV	257
DB	222	SHKFRVIAQGVELYTSDTAMHRPQVQATAVHKNESYDDKIYFFQENSHSDFKQPHTV	281
QY	258	SRVAQLCRGDQGGESSLSVSKWNTFLKMLVCSDAATNRNPNLQDVLLPDPSSGQWRD	317
DB	282	PRVQGVCSDDQGGESSLSVSKWNTFLKMLVCSDAATNRNPNLQDVLLPDPSSGQWRD	341
QY	318	RVYGVSPNPNYSACVYSLGDDIRVFTSSLAGYHMLSNRPNRPMCLPKQIPPTETFO	377
DB	342	LIYGLFLSPNPNYSACVYSLGDDIRVFTSSLAGYHMLSNRPNRPMCLPKQIPPTETFO	401
QY	378	VADSHPEVAQRV	389
DB	402	VADRYEVAQDPV	413

RESULT 2

G01856

semaphorin V - human

C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
C:Accession: G01856
R: Sekido, Y.
Submitted to the EMBL Data Library, June 1995
A:Reference number: G08634
A:Accession: G01856
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-749 <SEK>
A:Cross-references: EMBL:U28369; NID:g974283; PIDN:AA09138.1; PID:g974284
C:Superfamily: semaphorin

Query Match 17.4%; Score 368; DB 2; Length 749;
Best Local Similarity 28.9%; Pred. No. 8.1e-23;
Matches 127; Conservative 49; Mismatches 167; Indels 96; Gaps 18;

Qy 7 GRAAPSAPRARVLSLPARFGLRLRLRLVFWAAASAGHSRSPRISAVNKGQDHVDF 66
Db 22 GSAAPSPRLRL-----SFOELQA-WHGLQTESL 49
Qy 67 SOPEPHTVLFHEPGSFSVWVGKGVYHFNPEGKNASRVTVNI-----G 111
Db 50 ERTCCYQALLVDEERGLFVGAENHVASLNL---DNISKRAKKLAWPAPVWEWREECNWAG 106
Qy 112 STKGCQKQDCQGNVITLLER-RGNGLLVCGTNAARKPSC-----WNLVNDVVM-----SL 161
Db 107 KDIGT-----ECMNFVLLHAYNTHLLACGTGAFHPTCAFEVGHRAEPEVRLDPGR 161
Qy 162 GEMKGYAPFSPDENSILVFEDEVYSTIRKQYNGKIPFRFRIRGESELYT---SDTVMQ 218
Db 162 EDGKGKSPYDPRHRAASLVGEELYSVGAADLMGRDFTIFRSLGORPSLRTEPHDSRWLN 221
Qy 219 NPOFIKA-TIVHQDQAYDKIYFFREDNPDKNPE-APLNVSRVAQLCRGQGGESSLSV 276
Db 222 EPKVFVFWIPESNPDDDKIYFFRETFAVEAAPALGRLSVSRVQCICRNDVGGORS-LV 280
Qy 277 SKWNTFLKALVCS--DAATNRNENRLQDVFLLPDPSCQWRDTRVYGVFSNP---WNYS 331
Db 281 NKWNTFLKALVCSVPGVEGTHFDQLQDVLL---SSRDHRTPLLYAVFSSSIFQCSA 338
Qy 332 VCIVSLGDIRVF-----RTSSLKGYHMGSLNPRPGMCLPKK-----OPIPTE 374
Db 339 VCIVSMNDVRAFLGPFHKEGPMHGWVSYQGRVYPRPGMC-PSKTFGTFSSTKDFPD 397
Qy 375 TFQVADSHPEVAQRPEMG 393
Db 398 VIQFARNHPLMNSVLPNG 416

RESULT 3
D49423
semaphorin III precursor - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C:Accession: D49423
R: Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.
Cell 75, 1389-1399, 1993
A:Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone
A:Reference number: A49423; MUID:94094332; PMID:8269517
A:Accession: D49423
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-771 <KOL>
A:Cross-references: GB:L26081; NID:g799328; PIDN:AAA65938.1; PID:g436560
C:Genetics:
A:Gene: GDB:SEMA1
A:Cross-references: GDB:283448
C:Superfamily: semaphorin

Query Match 17.1%; Score 363; DB 2; Length 771;
Best Local Similarity 28.0%; Pred. No. 2.2e-22;
Matches 119; Conservative 66; Mismatches 162; Indels 78; Gaps 19;

Qy 32 RLLLVFWAAASAGHSRSG-----PRISAVNK-----GODHVDV-----SOPEPHTVLFHEP 79
Db 6 RIVCLFVGVLITARANYONGNNVPRKLKLSYKEMLESNNVITFNGLANSSSYHTFLDDEE 65
Qy 80 GSFSVWVGKGVYHFNPEGKNASRVTVNIGSTKGCQDK-----QDCGNYITLL 130
Db 66 RS-LUYVCAKDHIFFSFDLVNLIKDFQKIVMPVSYTR---RDECKWAGKDILKECANFIKVL 121
Qy 131 ER-RGNGLLVCGTNAARKPSC-----WNLVNDVVMVSLGEMKGYAPFSPDENS 176
Db 122 KAYNTHLYACGTGAFHPTCTYIEIGHHPEDNIEFKLENS---HFENGKSGSPYDKLLT 177
Qy 177 LVLEFEGDEVYSTIRKQYNGKIPFRFRIRGESELYT---SDTVMONPOFIKATIVHQ-DQ 232
Db 178 ASLLIDGELYSGTRAADFMRGFAIFRTLCHHHPIRTEQHDRSLWLNDRPFISAHLLISESDN 237
Qy 233 AYDKIYFFREDNPDKNPEAPLNVSRVAQLCRGQGGESSLSVSKWNTFLKAMLVCSDA 292
Db 238 PEDDKVYFFRENALDGEHSGKATHARIGQICKNDFGGHRS-LVNKWTTLKARLICSV 296
Qy 293 ATN---RNENLQDVLL--PDPSCQWRDTRVYGVF---SNPNYSACVYVSLGDIRVF 344
Db 297 GPNGIDTHFDQLQDVFLMNFKDP---KNPVYGVYFTTSSNIFKGSAYCMYSMSDVRVF 352
Qy 345 -----RTSSLKGYHMGSLNPRPGMCLPKK-----OPIPTETFOVADSHPEVAQ 387
Db 353 LGPVAHRDGNVQWVPYQGRVYPRPGTC-PSKTFEGDFDNDLPDDVITFARSHPAMYN 411
Qy 388 RVEPM 392
Db 412 PVFPM 416

RESULT 4
I48744
semaphorin A - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: I48744
R: Puschel, A.W.; Adams, R.H.; Betz, H.
Neuron 14, 941-948, 1995
A:Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creat
A:Reference number: I48744; MUID:95267431; PMID:7748561
A:Accession: I48744
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-748 <RES>
A:Cross-references: EMBL:X85990; NID:g854323; PIDN:CAA59982.1; PID:g854324
C:Genetics:
C:Superfamily: semaphorin

Query Match 17.1%; Score 361.5; DB 2; Length 748;
Best Local Similarity 29.9%; Pred. No. 2.9e-22;
Matches 133; Conservative 51; Mismatches 152; Indels 109; Gaps 23;

Qy 7 GRAAPSAPRARV--LSLPAREGL-PLRL-----RLLLV-----FWVAAASAQ 45
Db 22 GDTAPNLPRLRSLFQELQARHGVTFRLERTCCYEAALLVDEERGLFVGAENHVASLSLD 81
Qy 46 GHSRSGPRISAVNKGQDHVDFSQPEPHTVLFHEPGSFSVWVGKGVYHFNPEGKNASV 105
Db 82 NISKRAKLA--W-----PAPVWEWRECN---WAG----- 106
Qy 106 RTVNIGSTKGCQDKQDCGNYITLLRRGN-GLLVCGTNARKPSC---WNLVNDVVMVMS 160
Db 107 --KDGT-----ECMNFVLLHAYNTHLLACRTGAFHPTCALWRWATAGGTAST 155
Qy 161 ----LGEKMGYAPFSPDENSILVFEDEVYSTIRKQYNGKIPFRFRIRGESELYT---S 213
Db 156 GPEKLEDKGKGTYPDPRHPRPSVLVGEELYSVGTADLMGRDFTIFRSLGQNPSLRTEPHD 215

Qy	214	DTVMNQFIKA-TIVHQDAQYDDKIYYFFREDNPKNPE-APLNVSRVAQLCRGDQGG	271
Db	216	SRWLNEPKFKVFWPSESNPDODKIYFFRESAVEAAPMGMSVSRVGQICRNDLGGQ	275
Qy	272	SSLVSQWNTFLKAMLVCS--DAATNRNRLQDVLELLPDPSCQWRDT-RVYGVFSNP--	326
Db	276	RSL-VNKWTTFLKARLVCSVPVGGETHFDQLQDVLELL--SSRDQRTPLLVAVFSTSSG	331
Qy	327	-WNYSAVCVYSLGDIDRVF-----RTSSLKGYTHMGLSNRPDMGCIPLKK-----	368
Db	332	VFGSAYCVYSMNDVRAFLGLPLHKEGPTHQWVSYGGRVYPVRPGMC-PSKTFGTFSST	390
Qy	369	QPIPTETFEQVADSHPEVAQVPEPMG 393	
Db	391	KDPEDDVIQFGRNHPLMYNPVLPWG 415	
RESULT 5			
I48746			
semaphorin C - mouse (fragment)			
C:Species: Mus musculus (house mouse)			
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 03-Nov-2000			
C:Accession: I48746			
R:Puschel, A.W.; Adams, R.H.; Betz, H.			
Neuron 14, 941-948, 1995			
A:Title: Murine semaphorin D/collapsin is a member of a diverse gene family.			
A:Reference number: I48744; MUID:95267431; PMID:7748561			
A:Accession: I48746			
A:Status: preliminary;			
A:Molecule type: mRNA			
A:Residues: 1-782 <RES>			
A:Cross-references: EMBL:X85992; NID:g854327; PIDN:CAA59984.1; PID:g854328			
C:Genetics:			
A:Gene: semC			
C:Superfamily: semaphorin			

Query Match	16.8%;	Score	355.5;	DB	2;	Length	782;
Best Local Similarity	31.0%;	Pred. No.	9.8e-22;				
Matches	104;	Conservative	47;	Mismatches	138;	Indels	47;
Gaps	14;						
Qy	72	HTVLFEHPGGSVVMVGRGKYYHEN----	PPECKNASVRTVNI	LGSTKGSC-----	QDKQ	121	
Db	16	YTALLSQDGKTLVYGAREALFALNSL	SFLUPGGYQELLWSAD	RKQQCSFKGDKPKR	75		
Qy	122	DCGNYI--TLERRNGLLVCCTNARKPSC-----	WNLVND---	SVVMSLGEKMGYAPF	170		
Db	76	DCQNKIKILLPLNSSHLLTCGTA	AFSPLCAYIHIA	SFTLADEAGNVILEDG--	KGHC	133	
Qy	171	SPDENSILVFEGDEVYSTIRKQEVNGKIP	RRRIIRGESELYTSDTV--	MQNPQFIKATIV	228		
Db	134	DPNPKSTALVVDGJLE--TGTVSS	FGQNDPAISRQSSRP	TKTESSLNWLQDPAFV	192		
Qy	229	HODQAY---DDKITYYEFREDNPKNPE	APLVNSRVAOLCRGD	OGGESSLSVSKWNTLX	284		
Db	193	PESLGSPIGDDKIKYFFSETGGQFE	FPENTIVSRVARCKG	DGEGGERVIO--QRWTSFLK	251		
Qy	285	AMLVCSDAATNRNENRLQDVPELL--	PDPSGQWRDRFVYGV	FSNPWNY-----	SAYCVTSYLG	338	
Db	252	AQLLCSRPDDCGFPENVLQDVETL	PNPQ--DWRKTLIS	IGVFTV	SQWHRGTT	TEGSAICVFTMN	310
Qy	339	DIDRVF-----	RTSSLKGYHMLGN	SNRPGMCL	365		
Db	311	DVQKAFGLYKKVKNRETQOQWY	TETHOVPTPRPGACI	346			

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RESULT 6
A49069
collapsin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 24-Sep-1999
C:Accession: A49069
R:Luo, Y.; Raibite, D.; Raper, J.A.
Cell 75, 217-227, 1993

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A:Title: Collapsin: a protein in brain that induces the collapse and paralysis of neurons
A:Reference number: A49069; MUID:94006554; PMID:8402908
A:Accession: A49069
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-772 <LJ00>
A:Cross-references: GB:U02528; NID:g410078; PIDN:AAC59638.1; PID:g410079
C:Superfamily: semaphorin

Query Match	16.58;	Score	350;	DB	2;	Length	772;
Best Local Similarity	28.68;	Pred. No.	2.8e-21;				
Matches	123;	Conservative	56;	Mismatches	165;	Indels	86;
Gaps	19;						
Qy	29	LRLRLLLVFWAAASAOQHSRSGPRISAVWK	---	GQDHVDF	---	SOPEPHTVLVHEPG	80
Db	7	IALLSLVLLAGRVNCQHVKNVPRLLKLSYKEMLESNNIVNFNGLANSSSYHTFLDDEER	66				
Qy	81	SFSVWVGGRGVKVIYHNFPEGNKASVTVVNI	-----	GSTKGSQ	-----	DKQDCG	124
Db	67	S-RLYVGAKDHIFSNL	-----	VNIKEYOKI	VMPVSHSRDECKWAGKDLIRECA	115	
Qy	125	NYITLLER-RGNGLLVCGTNARKPKSCWNL	-----	VNDSVVMSLGEMGAPYPS	171		
Db	116	NFIKVLKTYNOTHLXACGTGAFHPCWYIEVGSHPEDNIFRMDS	---	HFENGGRKSPYD	172		
Qy	172	PDENSLVLFEGDEVYSTIRKOEYNGKIPRFRIRGESELYT	---	SDTVMQNPQIKATIV	228		
Db	173	PKLLTASLLVDGELYSGTAADFMRDEAIFRTLGHHPHPIRTEQHDRSLWLNDRPFIASHLI	232				
Qy	229	-HODQAVDDKIYTYFFREDNPDKNPEALNVSRVAQLCRGDGOGESSLSVSKWNTFLKAML	287				
Db	233	PESONPEDDKIYFFRENAIDGEHTGATHARIGCIKNDGFGHRSLL-VNKWTTFLKAL	291				
Qy	288	VCSDAATN----RNFENRLQDVPELL-PPDSQGMWRDTRYGVGF	---	SNPNWYS	SAVCVYSKLG	339	
Db	292	ICSVPGPNGIDTHEDELQDVFLMNSKDP	---	KNPIVYGVFTTSNFIKFGSAWCWYSMTD	347		
Qy	340	IDRVF-----RTSSLKGYHNGLSNPRGMCMLPKK	-----	QPIPETETQVADSH	382		
Db	348	VRRVFLGPIYAHRDGNPNQWVPYQGRVYPYPRPTC-PSKTFGFGFDSTKDLDPDEVITFAKSH	406				
Qy	383	PEVAQRVEPM	392				
Db	407	PAMYNPVFPI	416				

RESULT 7
I48747
semaphorin D - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision
C:Accession: I48747
R:Puschel, A.W.; Adams, R.H.; Betz, H.
Neuron 14, 941-948, 1995
A:Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creat
A:Reference number: I48744; MUID:95267431; PMID:7748561
A:Accession: I48747
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-772 <RES>
A:Cross-references: EMBL:X85993; NID:g854329; PIDN:CAA59985.1; PID:g854330
C:Genetics:
A:Gene: semD
C:Superfamily: semaphorin

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Query Match      16.5% Score 349; DB 2; Length 772;
Best Local Similarity 27.9%; Pred. NO. 3.4e-21;
Matches 117; Conservative 62; Mismatches 165; Indels 76; Gaps 19;

QY 36 VFVWAAAQAQGHRSRG---PRISAVWK---GDHVDVF-----SQPEPTVLTFHEPGSFS 83
    ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 10 LFWGVLLTARANYANGKNVVNRLKSLYSKEMLESNNVITFNGLANSSSYTHFLDDEERS-R 68
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QY 84 VWVGGGRKVVYHFNPEPEKKNASVRTVNTIGSTKGCQDK-----QDCGNYITLLER-R 133
Db 69 LYVGAKDHIFESNLNFKDKOKIWPVSYTR---RDECKWAGKDKILKECANFIKVLAYN 125
QY 134 GNCILLVCGTNAWKPSCNWL-----VNDSVVMSLGEKMGYAPFSPDENSLVLE 181
Db 126 QTHLYACGTGAFHPICTYIEVGHHPEDNIFKLODS---HFENGGRKSPYDPKLLTASLLI 182
QY 182 GDEVYSTIRKQEVNGKIPFRFRIRGESELYT---SDTVMQNPQFIKATV-HODQAYDDK 237
Db 183 DGELYSTADEFMCRDFAIFRTIGDHHPIRTEQHDSDRLNDPRFISAHLPESDNPEDDK 242
QY 238 IYVFFREDNPKNEAPLANVRAQLCRGQGGESSLSVSKWNTFLKAMLVCSDAATN-- 295
Db 243 VYFFERENAIAGEHSGKATHAIGQICKNDFGGHRSL-VNKWTTFLKARLICSVPNGI 301
QY 296 -RNFNRLODVLL--PPDSQWRDTRYGVF---SNPWNYSACVYSLGIDIRVF----- 344
Db 302 DTHFDELQDVFLMNSKDP---KNPIYGVFTTSSNIFKGSVCMYSMSDVRVFLGPYA 357
QY 345 ----RTSSLKGYHMLGNRPFGMCLPKK-----OPIPTETFOVADSHPEVAQRVEPM 392
Db 358 HRDGPYNQWVPYQGRVPYPRGTC-PSKTEGGFDSTKDLDDVITFGSRHPAMYNVPPI 416

RESULT 8

S29921

hypothetical protein 15 - vaccinia virus

C:Species: vaccinia virus

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999

R:Accession: S29921

submitted to the EMBL Data Library, January 1991

A:Reference number: S29907

A:Accession: S29921

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-441 <AME>

A:Cross-references: EMBL:X57318; NID:g62239; PIDN:CAA40587.1; PID:g62254

Query Match

16.1%; Score 341.5; DB 2; Length 441;

Best Local Similarity 31.1%; Pred. No. 6.7e-21;

Matches 98; Conservative 51; Mismatches 127; Indels 39; Gaps 14;

QY 84 VWVGGGRKVVYHFNPEPEKKNASVRTVNTIGSTKGCQDKQDCGNYITL---LERRNGLLVC 140
Db 74 LYTGVGNAVYTF-----NNKLNT---GLTN-----NNYITTSIKVEDADKDTLVC 117

QY 141 GTNARKPSCNWLNDVSVSLGEMKGYAPFSPDENSLVLEFEGDEVYSTIRKQYNGKIPR 200
Db 118 GTNNGNPKCKWKIDGSDDPKHG--RGYAPYQNSKVTIISHNGC-VLSDINISKEG--IKR 172

QY 201 FRRIRGES--ELVTSVTMQNPQFIKATVHQDAQYDDKIYFFREDNPKNPEAPLNV 258
Db 173 WRRFDGPGCYDLYTADNVIPK-DGLRGAFVDKGTY-DKVVILFTDTIGSKR---IVKIP 227

QY 259 RVAQLCRGDOGGESSLSVSKWNTFLKAMLVCS-DAATNRNFRNLQDVFLPDPGSGWRDT 317
Db 228 YIAQMLCNDEGGPSSLSHRWSTFLKVELECDIDGRSYROI--IHSRTIKTD-----NDT 280

QY 318 RVYGVFSNPWNYSAVCVYSLGIDIRVFTSSLKGYHMLGNRPFGMCLPKKQPIPTETFO 377
Db 281 ILVFFDPSYKSALCTYSMTIKQSPSTSKLEGYTKQLPSPASGICLPAGKVVPHHTFE 340

QY 378 VADSHPEVAQRVEPM 392
Db 341 VIEKYNVLDDIIRKPL 355

RESULT 9

E42521

A39R protein - vaccinia virus (strain Copenhagen)

C:Species: vaccinia virus

A:Note: host Homo sapiens (man)

C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 08-Apr-1994

C:Accession: E42521

R:Johnson, G.P.

submitted to GenBank, June 1990

A:Reference number: A33172

A:Accession: E42521

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-403 <JOH>

Query Match

16.1%; Score 340.5; DB 2; Length 403;

Best Local Similarity 30.8%; Pred. No. 7.1e-21;

Matches 97; Conservative 53; Mismatches 126; Indels 39; Gaps 14;

QY 84 VWVGGGRKVVYHFNPEPEKKNASVRTVNTIGSTKGCQDKQDCGNYITL---LERRNGLLVC 140
Db 36 LYTGVGNAVYTF-----NNKLNT---GLTN-----NNYITTSIKVEDADKDTLVC 79

QY 141 GTNARKPSCNWLNDVSVSLGEMKGYAPFSPDENSLVLEFEGDEVYSTIRKQYNGKIPR 200
Db 80 GTNNGNPKCKWKIDGSDDPKHG--RGYAPYQNSKVTIISY-NECVLSDINISKEG--IKR 134

QY 201 FRRIRGES--ELVTSVTMQNPQFIKATVHQDAQYDDKIYFFREDNPKNPEAPLNV 258
Db 135 WRRFDGPGCYDLYTADNVIPK-DGLRGAFVDKGTY-DKVVILFTDTIGSKR---IVKIP 189

QY 259 RVAQLCRGDOGGESSLSVSKWNTFLKAMLVCS-DAATNRNFRNLQDVFLPDPGSGWRDT 317
Db 190 YIAQMLCNDEGGPSSLSHRWSTFLKVELECDIDGRSYROI--IHSRTIKTD-----NDT 242

QY 318 RVYGVFSNPWNYSAVCVYSLGIDIRVFTSSLKGYHMLGNRPFGMCLPKKQPIPTETFO 377
Db 243 ILVFFDPSYKSALCTYSMTIKQSPSTSKLEGYTKQLPSPAGICLPAGKVVSHHTFE 302

QY 378 VADSHPEVAQRVEPM 392
Db 303 VIEKYNVLDDIIRKPL 317

RESULT 10

I48748

semaphorin E - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C:Accession: I48748

R:Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995

A:Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creat

A:Reference number: I48744; MUID:95267431; PMID:7748561

A:Accession: I48748

A:Status: preliminary; translated from GB/EMBL/DDDBJ

A:Molecule type: mRNA

A:Residues: 1-751 <RES>

A:Cross-references: EMBL:X85994; NID:g854331; PIDN:CAA59986.1; PID:g854332

C:Genetics:

A:Gene: seme

C:Superfamily: semaphorin

Query Match

15.6%; Score 331.5; DB 2; Length 751;

Best Local Similarity 26.2%; Pred. No. 9.9e-20;

Matches 108; Conservative 68; Mismatches 178; Indels 59; Gaps 16;

QY 33 LLLVFWAAASAGHSRSGPRISAVW-----KQDHVDFS-QPEPHTVLFEHPGFSVW 85
Db 8 VLVGVFICSTCVRGSSQPOQARVYLTDELRETKTSETFSLSHQOLDRIILIMDEDDQRIY 67

QY 86 VGGRGKVVYHFNPEPEKKNAS-----VRTVNTIGSTKGCQD-KQDCGNYITLLER-RG 134
Db 68 VGSKDHLISLNI---NNISQELSVFVWPASTIKVECKMAGKDPHTGCGNFVRVIOQTNR 124

QY 135 NGLLVCGTNARKPCSNWL-----VNDSVW---SLGEMKGYAPFSPDENSLVLEFEGDEV 186
Db 135 NGLLVCGTNARKPCSNWL-----VNDSVW---SLGEMKGYAPFSPDENSLVLEFEGDEV 186

Db 125 THLYVCGGAFSPVCTYLNRRSRSDQVFMIDSKCSGKGRCSFNPVNTVSMINEELF 184
QY 187 STIRKQYNGKIPRRIRIRGESELYT---SDTVMQNQPIKATIVHQ-DQAYDDKITYYFF 242
Db 185 SGMYIDFMGTDAIFSLTKRQLRTDQHNKWLSPMFVDAHVDPDGTDPNDKAYVYFF 244
QY 243 REDNPKNPEAPLNVSRAQLCGDGGESSLSVSKWNTFLKAMLVCS---DAATNRNFN 299
Db 245 KERLTDNNRSTKQIHSMIARICPNDTGGQORSL-VNKWTTFLKARLVCSVTDEGGPETHD 303
QY 300 RLQDVFLPDPGQWRDTRVYGVF---SNPNYSAVCVYSLGDIIDRVFR-----TS 347
Db 304 ELEDVFLLETDNP--RTTLVGIPTTSSSVFKGSACVYVHLSDIQVFNFGFAHKBGPNH 361
QY 348 SLKGYHMGSLNPRPGMC-----LPKKQPIPTETFEQVADSHPEVAQVPEM 392
Db 362 QLISQGRIPYPRPGTCGCAFTPNMRTKDPDDVVTVTIRNHLPMYNSISPI 414
RESULT 11
S66498
semaphorin III - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Sep-1999
C:Accession: I58169
R:Wessersmith, E.K.; Leonardo, E.D.; Shatz, C.J.; Tessier-Lavigne, M.; Goodman, C.S.; K
Neuron 14, 949-959, 1995
A:Title: Semaphorin III can function as a selective chemorepellent to pattern sensory pr
A:Reference number: I58169; MUID:95267432; PMID:7748562
A:Accession: I58169
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-666 <RES>
A:Cross-references: GB:L40484; NID:g703189; PIDN:AAA73934.1; PID:g703190
C:Genetics:
A:Gene: SemalIII
C:Superfamily: semaphorin
Query Match 15.5%; Score 329.5; DB 2; Length 666;
Best Local Similarity 31.3%; Pred. No. 1.2e-19;
Matches 100; Conservative 42; Mismatches 116; Indels 61; Gaps 14;
QY 121 QDCGNVITLLER-RGNGLLVCGTNAKPCSWNL-----VNDSSVMSLGMKGY 167
Db 6 KECANFIKVLVYANQTHLYACGTGAHPICITYIEGVHHPEDNIFKLODS---HFENGRGK 62
QY 168 APSPDENSLVLPFGDEVYSTIRKQYNGKIPRRIRIRGESELYT---SDTVMQNQPIK 224
Db 63 SPYDKLLTASLLIDGELYSGTAANPMGRDFAIFRTLGHHPHPIRTHQHDSRWLNDPRTS 122
QY 225 ATIV-HQDQAYDDKIYFFREDNPKNPEAPLNVSRAQLCRDQGGESSLSVSKWNTFL 283
Db 123 AHLIPESDNPEDDKVYFFFRNADGEHSGKATHARIGQICRKNDFGGHRS-L-VNKKWTTFL 181
QY 284 KAMLVCSDAATN---RNFNRQLQDVFL--PDPSGQWRDTRVYGVF---SNPNYSAVCVY 335
Db 182 KARLICSVPGPNGIDTHFDLQDVFLMNSKDP----KNPIVYGVFTTSSNIFKGSACVY 237
QY 336 SLGDDIRVFRSSLK-----YHMGSLNPRPGMCLPKK-----QPIPT 373
Db 238 SMSDVRV-----LLGPYAHRDGPNYQWVYQGRVYPRPGTC-PSKTFGGFDSTKDLPD 291
QY 374 ETFOVADSHPEVAQVPEM 392
Db 292 DVITFARSHPAMVNPVFI 310

RESULT 12
G02173
semaphorin III family homolog - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
C:Accession: G02173

R: Naylor, S.
submitted to the EMBL Data Library, October 1995
A:Reference number: G09275
A:Accession: G02173
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-753 <NAV>
A:Cross-references: EMBL:U38276; NID:g1061350; PIDN:AAB18276.1; PID:g1061351
C:Superfamily: semaphorin
Query Match 15.4%; Score 327.5; DB 2; Length 753;
Best Local Similarity 26.4%; Pred. No. 2.2e-19;
Matches 114; Conservative 63; Mismatches 162; Indels 93; Gaps 19;
QY 20 SLPAREGLPLRLRLLLVFWVAASAQGH-----SRSGPRISAVWKGDH----- 63
Db 19 SFTQDHLTPATPKRVLSFKELKATGTAHFNFLLNTDYRI--LLKDEDDHRYVSGKDY 76
QY 64 --VDFSQPEPHTVLFHEPGSFSVWVGGRGVYHFNFPKGNASVTVNIGSTKGCQDK 120
Db 77 VLSDLHDINREPLIHH-----WAASQRI-----ECVLSGKDVN----- 112
QY 121 QDCGNVITLLER-RGNGLLVCGTNAKPCSWNLV-----DSVVM-----SLGEMKGYAP 169
Db 113 GECGNEVRLIQPNWRTHLVYCGGTAYNPMC-TVYNGRRRAQDYIFYLEPERLESKGKCP 171
QY 170 FSPDENSLVLPFGDEVYSTIRKQYNGKIPRRIRIRGESELYT---SDTVMQNQPIKAT 226
Db 172 YDPKLTASALINEELYAGYIDFMGTAAIFRTLGKQTAMRTDQYNRWLNDPSTIAE 231
QY 227 IVHQDQAYDDKIYFFREDNPKNPEAPLNVSRAQLCRDQGGESSLSVSKWNTFLKAM 286
Db 232 LIPDSAEENDKLYFFFRERSAEA-POSPAVYARIGRICLNDGCGHCL-VNKKWSTFLKAR 289
QY 287 LVCS-----DAATNRFNRQLQDVFLPDPGQWRDTR---VYGVFSPNP---WNYSAVCVYSL 337
Db 290 LVCSVPGDGIETHFDLQDVVF-----QQTQDVNRVPIYAVFTSGSVFRGSVAVCYSM 344
QY 338 GDIDRVFR-----TSSLKGYHMGSLNPRPGMC-----LPKKQPIPTETFOVAD 380
Db 345 ADIRMYVGFPGFAHKEGPNYQWMPFGSKMPYPRGTCPGGTFTPTSMKSTKDYDPEVNFMR 404
QY 381 SHPEVAQVPEM 392
Db 405 SHPLMYQAVYPL 416
RESULT 13
S66498
M-sema F protein precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 24-Nov-1999
C:Accession: S66498
R:Inagaki, S.; Furuyama, T.; Iwashashi, Y.
FEBS Lett. 370, 269-272, 1995
A:Title: Identification of a member of mouse semaphorin family.
A:Reference number: S66498; MUID:95385809; PMID:7656991
A:Accession: S66498
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-834 <INA>
A:Cross-references: EMBL:S79463; NID:g1110598; PIDN:AAB35184.1; PID:g1110599
C:Superfamily: semaphorin
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-834/Product: M-sema F protein #status predicted <MAT>
Query Match 14.8%; Score 314; DB 2; Length 834;
Best Local Similarity 27.8%; Pred. No. 3.5e-18;
Matches 98; Conservative 50; Mismatches 149; Indels 56; Gaps 12;
QY 84 VWVGRGKYYHFN-----PECKNASVTVNIGSTKGCQDKQDCGNVITLL 130
Db 65 LYVGAREALFAFSVEALELQGAISWEAPAEK-----KIECTKGKSNTECFIRFL 117

Qy 131 E-RRGNGLLVCGTNARKSCNWLNVDSVVMSLGEV---KGYAPFSPDENSELVFEGDEVY 186
Db 118 QPYNSSHLVGYCGTAFQPKCTYINMLTFLDRAEPEDGKCPYPDKAGHTGLLLVDGELY 177
Qy 187 STIRKQEVNGKIPFRFRTIRGESELYTSDTV---MONPOFIKATIVHOD---QAYDDKIY 239
Db 178 SA-TLNNFLGTPEVILRVNGTHHSIKTYLAFWLNEPHFVGSAFVPSVSGFTGDDDKIY 236
Qy 240 YFFREDNPDKNPEAPLVNSYQAOLCRGDQGGESSLSVKWNTFLKAMLVCSDAATNRNFN 299
Db 237 FFFSERAVEYDCYSEQVVVARVCKGDMGCGARTLQ-KKWTTLKARLVCSAPDKWKVYFN 295
Qy 300 RLQDVFLLPDSGQWRDTRVYGVFSNPW---NYSACVSVYSGDDIRVF-----RTS 347
Db 296 QLKAVHTLIRGAS---WHNITTFGVFQARMGDMDL SAVCEYQLQIQOVPEGPKYKEYSEQA 353
Qy 348 SLKGYHMGSLNPRPGMCL-----PKKQPIPTETFOVADSHPEVAQVRPEP 391
Db 354 KWARYTDVPSPRGSCINWHRDNGYTSLELFDNTLNFITKKHPLMEDQVKP 406

RESULT 14

JH0798

fasciclin IV precursor - American bird grasshopper

C:Species: Schistocerca americana (American bird grasshopper)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: JH0798

R:Kolodkin, A.; Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Goodenough, R. 1992

A:Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance in the developing central nervous system

A:Reference number: JH0798; MUID:93040225; PMID:1418998

A:Accession: JH0798

A:Molecule type: mRNA

A:Residues: 1-730 <XOL>

A:Cross-references: GB:L00709; NID:g160844; PID:g160845

A:Experimental source: embryo

C:Comment: This protein plays a role in growth cone guidance in the developing central nervous system

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-730/Product: fasciclin IV #status predicted <NAT>

F:23-627/Domain: extracellular #status predicted <EXT>

F:628-652/Domain: transmembrane #status predicted <TM>

F:653-730/Domain: intracellular #status predicted <INT>

F:44,71,163,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.7%; Score 312; DB 2: Length 730;
Best Local Similarity 28.9%; Pred. No. 4.2e-18;
Matches 114; Conservative 57; Mismatches 165; Indels 58; Gaps 19;

Qy	29	LRURLLLV--FWAAASAGHSRSGPRISAVMKGODHVD-FSQPEPHTVLPH--EPGSF 82
Db	1	MRAALVAVALLWALHAAAWNDVSPKM-VYQGEERVQRLGNESHKDHFKLLEKDH 59
Qy	83	SVWVGGRKVVYHNFPEGKNASVPTVNIQST-----KGCQDKQDCQGNITLLER- 132
Db	60	SLVGARNIVYNISLRLDTEFTQRIEWHSSGAHRELCYLKGSED--DCQNTIRVLAKI 117
Qy	133	RGNGLLVCGFNARKPSCWNLV--NSVVMSLGEMKGYAPFSDENSLVLFCGEDEVYSTI 189
Db	118	DDRVLCIGGNAYKPCRHYALXKGDGYVVEKEYEGLGCLPFDPDHNNSTAIYSEGQLYSA- 176
Qy	190	RKOEYNGKIPRRIRIGESELYTSDTVMQN-POFIKATIVHQDQAYDDKITYFREDNPD 248
Db	177	TVADFSTGPLI--YRGPLRTESDLKQLNAPFVNT-----MEYNDIFFEFPRETAVE 228
Qy	249	KNPEAPLNTSVRAQLCGDQGOESSLSVKWNFTLKAMLYCSDAATNR-NFNRLQDVF-L 306
Db	229	YINCGKAIYSRVARVCKHDKGPPHQEG-DRWTFSLKSLNCSVPGDYPFVNEIQSTSDI 287
Qy	307	LPDPSGQWRDTRYGVFSNPWNY---SANCVYSLGDI----DRVR-----TSS 348
Db	288	IEGNYGGVEKLLYGVFTTPVNSIGGSVACASMKSILESFQDGPFFKEQETMNSNLVAPS 347

Qy 349 LKGVHMGSLNRPNGMCLPKPKQIPITETQVADSH 382
|| : ||||| : : : ||
Db 348 LK-----VPEPRPGQCVNDSRTLDPVSVNFVKSH 376

RESULT 15

A49423
semaphorin I precursor - beetle (Tribolium confusum)
C:Species: Tribolium confusum
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C:Accession: A49423
R:Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.
Cell 75, 1389-1399, 1993
A:Title: The Semaphorin genes encode a family of transmembrane and secreted growth co
A:Reference number: A49423; MUID:94094332; PMID:8269517
A:Accession: A49423
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: mRNA
A:Residues: 1-711 <KOL>
A:Cross-references: GB:L26080

```

Query Match      14.1%; Score 298; DB 2; Length 711;
Best Local Similarity 29.4%; Pred. No. 6.2e-17;
Matches 102; Conservative 55; Mismatches 134; Indels 56; Gaps 18;

QY 72 HTVLFEHPGCSFVWVGGRKYYH---FNFPGKNASVFTVNIQS-----TKGSCQDKQD 122
   | : : : : : | | | | : | | : : : : : | | : | |
Db 48 HFVLNQDET-SILVGGRRNYNLSIFDLSEKRGGRIDWPSSDAHGQLCILKGTDD--D 104
   | : : : : : | | | | : | | : : : : : | | : | |
QY 123 CGNVIITLLERRNG-LIVCGFNARKPSGWN-----LVNDSVVMSLGEMKGVAPFSPD 173
   | : : : : : | | | | : | | : : : : : | | : | |
Db 105 QCNVIRILYSEPKLVICGNSVKPLCRTYAFEGKYLVEKV-----EGIGLCYPNPE 159
   | : : : : : | | | | : | | : : : : : | | : | |
QY 174 ENSL-VLFEQDEVYSTIRKQBYNKGKIPFRFRIGESELYTSDTYNQN-PQFIKATIVHQD 231
   | | : : : : : | : : : : : | | : : : : : | | : | |
Db 160 HNSTSVSYNGOLFSAIV-ADFSGDPLIYREPORTEL--SDLQOLNAPNEVNSV----- 210
   | : : : : : | : : : : : | | : : : : : | | : | |
QY 232 QAYDDKLYYFREDNPDKNPAPLNVSRVAQLCRDQGGESSLSVSKWNTFLKAMLVCS- 290
   | | : : : : : | : : : : : | | : : : : : | | : | |
Db 211 -AYGDYIFFFYRETAYEMNGKVIYSRVACGKDDKGGPHQ-SRDRTWSFLKALNCISI 268
   | : : : : : | : : : : : | | : : : : : | | : | |
QY 291 DAATNRNFRLQDVFLLPDPFSQGWDRTR-VYGVFSNPWNV---SAVCVYSGLGDIRVERT 346
   | : : : : : | : : : : : | | : : : : : | | : | |
Db 269 PGEYFPFYDEIQSTSDIVEGRYNSDDSKIIYILTPVNAIGGSAICAYQADILRVFE- 327
   | : : : : : | : : : : : | | : : : : : | | : | |
QY 347 SSLKGYHMGUSN-----PRPGMCLPKKQIPETPTQVADSH 382
   | | : : : : : | | | | : : : : : | | : | |
Db 328 GSFKHQETINSMLVPQNLVPERPGQCVDRSDRILPDKNNVFIKTH 374

```

Search completed: March 14, 2003, 09:27:45
Job time : 16.5226 secs